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APR 2

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1600

#31

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/267,963D

DATE: 04/18/2003

TIME: 14:22:06

Input Set : N:\CrF4\04072003\I267963B.raw

Output Set: N:\CRF4\04182003\I267963D.raw

1 <110> APPLICANT: MIYAZONO, Kohei
 2 IMAMURA, Takeshi
 3 DEN DIJKE, Peter
 4 <120> TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS,
 CORRESPONDING

5 NUCLEIC ACID MOLECULES AND THEIR USE
 6 <130> FILE REFERENCE: LUD 5539.1 CIP
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/267,963D
 8 <141> CURRENT FILING DATE: 1999-03-12
 9 <150> PRIOR APPLICATION NUMBER: PCT/GB93/02367
 10 <151> PRIOR FILING DATE: 1993-11-17
 11 <150> PRIOR APPLICATION NUMBER: US 09/039,177
 12 <151> PRIOR FILING DATE: 1998-03-13
 13 <160> NUMBER OF SEQ ID NOS: 46

14 <170> SOFTWARE: PatentIn version 3.2
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1984
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 20 <400> SEQUENCE: 1

ENTERED

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| 22 | agaaacattt ttgctccagc ccccatccca gtcccggag gctgccgcgc cagctgcgcc | 120 |
| 23 | gagcgagccc ctccccggct ccagccgggt ccggggccgc gccggacccc agccgcgg | 180 |
| 24 | ccagcgctgg cggtgcaact gcggccgcgc ggtggagggg agtgtggccccc gttccgcga | 240 |
| 25 | aggctagcgc cccgccaccc gcagagcggg cccagaggga ccatgacctt gggctccccc | 300 |
| 26 | aggaaaggcc ttctgtatgtc gctgtggcc ttgtgtaccc agggagaccc tgtgaagccg | 360 |
| 27 | tctcggggcc cgctgggtac ctgcacgtgt gagagccac attgcaaggg gcctacctgc | 420 |
| 28 | cggggggcct ggtgcacagt agtgcgtggc cgggaggagg ggaggcaccc ccaggaacat | 480 |
| 29 | cgggctgcg ggaacttgca cagggagctc tgcagggggc gcccccacca gttcgtcaac | 540 |
| 30 | cactactgct gcgcacagcca cctctgcaac cacaacgtgt ccctgggtct ggaggccacc | 600 |
| 31 | caacctccctt cggagcagcc gggAACAGAT ggccagctgg ccctgatcct gggcccccgtg | 660 |
| 32 | ctggccttgc tggccctgggt ggccttgggt gtccctggcc tggcatgt ccgacggagg | 720 |
| 33 | caggagaagc agcgtggcct gcacagcgg ctggagagt ccagtctcat cctgaaagca | 780 |
| 34 | tctgagcagg gcgcacacgt gttgggggac ctccctggaca gtgactgcac cacagggagt | 840 |
| 35 | ggctcagggc tccccttcctt ggtgcagagg acagtggcac ggcagggtgc cttggggag | 900 |
| 36 | tgtgtggaa aaggccgcta tggcgaagt tggcgggct tggcacgg tgagagtgtg | 960 |
| 37 | gccgtcaaga tcttctccctc gagggatgaa cagtcctgggt tccgggagac tgagatctat | 1020 |
| 38 | aacacagtat tgctcagaca cgacaacatc ctaggctca tcgcctcaga catgacccctcc | 1080 |
| 39 | cgcaactcga gcacgcagct gtggctcat acgcactacc acgagcacgg cttcccttcac | 1140 |
| 40 | gactttctgc agagacagac gctggagccc catctggctc tgaggctacg tggccgcgc | 1200 |
| 41 | gcatgcggcc tggcgcaccc gcacgtggag atcttcggta cacagggcaa accagccatt | 1260 |
| 42 | gcccaccgcg acttcaagag ccgcaatgtg ctggtaaga gcaacctgcg gtgtgcac | 1320 |
| 43 | gccgacctgg gcctggctgt gatgcactca cagggcagcg attacctgga catcgcaac | 1380 |
| 44 | aacccgagag tggcaccacaa gcgtacatg gcacccgagg tgctggacga gcagatccgc | 1440 |

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Input Set : N:\CrF4\04072003\I267963B.raw
 Output Set: N:\CRF4\04182003\I267963D.raw

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| 45 | acggactgct ttgagtccctaa caagtggact gacatctggg cctttggcct ggtgtgtgg | 1500 |
| 46 | gagattgccc gccggaccat cgtgaatggc atcgtggagg actatacgacc acccttctat | 1560 |
| 47 | gatgtgggtgc ccaatgaccc cagcttttag gacatgaaga aggtgggtgtg tgtggatcag | 1620 |
| 48 | cagacccccc ccataccctaa ccggctggct gcagacccgg tcctctcagg cctagtcag | 1680 |
| 49 | atgtatgcggg agtgctggta cccaaacccc tctgcccac tcaccgcgct gcggatcaag | 1740 |
| 50 | aagacactac aaaaaattag caacagtcca gagaaggcta aagtgttca atagccagg | 1800 |
| 51 | agcacctgat tcctttctgc ctgcaggggg ctgggggggt gggggggcagt ggatggtgcc | 1860 |
| 52 | ctatctgggt agaggtatgt tgagtgtgggt gtgtgtggg gatggggcagc tgccctgccc | 1920 |
| 53 | tgctcgcccc ccagcccacc cagccaaaaa tacagctggg ctgaaaacctg aaaaaaaaaaa | 1980 |
| 54 | aaaaa | 1984 |
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| 57 | <211> LENGTH: 503 | |
| 58 | <212> TYPE: PRT | |
| 59 | <213> ORGANISM: Homo sapiens | |
| 60 | <400> SEQUENCE: 2 | |
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| 63 | Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val | |
| 64 | 20 25 30 | |
| 65 | Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly | |
| 66 | 35 40 45 | |
| 67 | Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln | |
| 68 | 50 55 60 | |
| 69 | Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg | |
| 70 | 65 70 75 80 | |
| 71 | Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn | |
| 72 | 85 90 95 | |
| 73 | His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln | |
| 74 | 100 105 110 | |
| 75 | Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala | |
| 76 | 115 120 125 | |
| 77 | Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg | |
| 78 | 130 135 140 | |
| 79 | Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser | |
| 80 | 145 150 155 160 | |
| 81 | Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp | |
| 82 | 165 170 175 | |
| 83 | Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe | |
| 84 | 180 185 190 | |
| 85 | Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val | |
| 86 | 195 200 205 | |
| 87 | Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu | |
| 88 | 210 215 220 | |
| 89 | Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe | |
| 90 | 225 230 235 240 | |
| 91 | Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile | |
| 92 | 245 250 255 | |
| 93 | Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln | |
| 94 | 260 265 270 | |

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Input Set : N:\CrF4\04072003\I267963B.raw
 Output Set: N:\CRF4\04182003\I267963D.raw

95 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
 96 275 280 285
 97 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
 98 290 295 300
 99 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
 100 305 310 315 320
 101 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
 102 325 330 335
 103 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
 104 340 345 350
 105 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
 106 355 360 365
 107 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
 108 370 375 380
 109 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
 110 385 390 395 400
 111 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
 112 405 410 415
 113 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
 114 420 425 430
 115 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
 116 435 440 445
 117 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
 118 450 455 460
 119 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
 120 465 470 475 480
 121 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
 122 485 490 495
 123 Glu Lys Pro Lys Val Ile Gln
 124 500
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 127 <211> LENGTH: 2724
 128 <212> TYPE: DNA
 129 <213> ORGANISM: Homo sapiens
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 132 gactgtgggc agatgtgacc aagagcctgc attaagttgt acaatggtag atggagtgtat 120
 133 gattcttcct gtgttatca tgattgtct cccctccccct agtatggaa atgagaagcc 180
 134 caaggtcaac cccaaactct acatgtgtgt gtgtgaaggt ctctcctgcg gtaatgagga 240
 135 ccactgtgaa ggccagcagt gctttccctc actgagcatc aacgatggct tccacgtcta 300
 136 ccagaaaaggc tggttcagg ttatgagca gggaaagatg acctgtaaaga ccccgccgtc 360
 137 ccctggccaa gctgtggagt gctgccaagg ggactgggt aacaggaaca tcacggccca 420
 138 gctgccact aaaggaaaat cttccctgg aacacagaat ttccacttgg agttggcct 480
 139 cattattctc tctgttagtgt tcgcagtatg tcttttagcc tgcctgctgg gagttgtct 540
 140 ccgaaaattt aaaaggcgca accaagaacg cctcaatccc cgagacgtgg agtatggcac 600
 141 tatcgaagggt ctcatcacca ccaatgttg agacagcact ttagcagatt tattggatca 660
 142 ttctgttaca tcaggaagt gctctggct tcctttctg gtacaaagaa cagtggctcg 720
 143 ccagattaca ctgttggagt gtgtcggaa aggcaaggat ggtgaggtgt ggagggcag 780
 144 ctggcaaggg gaaaatgttg ccgtgaagat cttctccctcc cgtgatgaga agtcatggtt 840

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Input Set : N:\CrF4\04072003\I267963B.raw
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| 146 | tgcctcagac | atgacatcaa | gacactccag | tacccagctg | tggttaatta | cacattatca | 960 | | | | | | | | | | |
| 147 | tgaaatggga | tcgttgtagc | actatctca | gcttactact | ctggatacag | ttagctgcct | 1020 | | | | | | | | | | |
| 148 | tcaaatagtg | ctgtccatag | ctagtggct | tgcacatgg | cacatagaga | tattgggac | 1080 | | | | | | | | | | |
| 149 | ccaaggaaa | ccagccattg | cccatcgaga | tttaaagagc | aaaaatattc | tggttaagaa | 1140 | | | | | | | | | | |
| 150 | gaatggacag | tgttgcatag | cagatttggg | cctggcagtc | atgcattccc | agagcaccaa | 1200 | | | | | | | | | | |
| 151 | tcaagtttat | gtggggaaaca | atccccgtt | gggcaccaag | cgctacatgg | cccccaagt | 1260 | | | | | | | | | | |
| 152 | tctagatgaa | accatccagg | tgattgttt | cgattcttat | aaaagggtcg | atatttggc | 1320 | | | | | | | | | | |
| 153 | cttggactt | gttttgggg | aagtggccag | gcggatggtg | agcaatggta | tagtggagga | 1380 | | | | | | | | | | |
| 154 | ttacaagcca | ccgttctacg | atgtggttcc | caatgaccca | agttttgaag | atatgaggaa | 1440 | | | | | | | | | | |
| 155 | ggtagtctgt | gtggatcaac | aaaggccaaa | cataaccaac | agatggttct | cagacccgac | 1500 | | | | | | | | | | |
| 156 | attaacctct | ctggccaagc | taatgaaaga | atgctggat | aaaaatccat | ccgcaagact | 1560 | | | | | | | | | | |
| 157 | cacagcaactg | cgtatcaaaa | agactttgac | caaaattgtat | aattccctcg | acaaattgaa | 1620 | | | | | | | | | | |
| 158 | aactgactgt | tgacattttc | atagtgtcaa | gaaggaagat | ttgacgttgt | tgtcattgtc | 1680 | | | | | | | | | | |
| 159 | cagctggac | ctaattgtgg | cctgactgg | tgtcagaatg | gaatccatct | gtctccctcc | 1740 | | | | | | | | | | |
| 160 | ccaaatggct | gctttgacaa | ggcagacgtc | gtaccagcc | atgtgttggg | gagacatcaa | 1800 | | | | | | | | | | |
| 161 | aaccacccta | acctcgctcg | atgactgtga | actggcatt | tcacgaactg | ttcacactgc | 1860 | | | | | | | | | | |
| 162 | agagactaat | gttggacaga | cactgttgca | aaggtaggaa | ctggaggaac | acagagaaat | 1920 | | | | | | | | | | |
| 163 | cctaaaagag | atctggcat | taagtcaagt | gctttgcata | gctttcacaa | gtctccctaga | 1980 | | | | | | | | | | |
| 164 | cactccccac | gggaaactca | aggaggtgg | gaattttaa | ttagcaatat | tgcctgtgct | 2040 | | | | | | | | | | |
| 165 | tctcttcttt | attgcactag | gaattctttt | cattccttac | ttgcactgtt | actcttaatt | 2100 | | | | | | | | | | |
| 166 | ttaaagaccc | aacttgccaa | aatgttggct | gcgtactcca | ctggctctgtc | tttgataat | 2160 | | | | | | | | | | |
| 167 | aggaattcaa | tttggcaaaa | aaaaatgtaa | tgtcagactt | tgctgcattt | tacacatgtg | 2220 | | | | | | | | | | |
| 168 | ctgatgttta | caatgatgcc | gaacatttagg | aattgtttat | acacaacttt | gcaaattatt | 2280 | | | | | | | | | | |
| 169 | tattacttgt | gcacttagta | gttttacaa | aactgctttg | tgcataatgtt | aaagcttatt | 2340 | | | | | | | | | | |
| 170 | tttatgtggt | ctttagtattt | tattacagaa | atgtttttaa | cactataactc | taaaatggac | 2400 | | | | | | | | | | |
| 171 | attttctttt | attatcagtt | aaaatcacat | tttaagtgt | tcacattttgt | atgtgtgttag | 2460 | | | | | | | | | | |
| 172 | actgtaactt | tttttcagtt | catatgcaga | acgtatttag | ccattaccca | cgtgacacca | 2520 | | | | | | | | | | |
| 173 | ccgaatatat | tatcgattta | gaagcaaaga | tttcagtaga | attttagtcc | tgaacgctac | 2580 | | | | | | | | | | |
| 174 | ggggaaaatg | cattttcttc | agaattatcc | attacgtgca | ttttaactct | gccagaaaaaa | 2640 | | | | | | | | | | |
| 175 | aataactatt | ttgttttaat | ctactttttt | tattnagtag | ttattngtat | aaattaaata | 2700 | | | | | | | | | | |
| 176 | aactgttttc | aagtcaaaaa | aaaa | | | | 2724 | | | | | | | | | | |
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| 185 | Pro | Ser | Pro | Ser | Met | Glu | Asp | Glu | Lys | Pro | Lys | Val | Asn | Pro | Lys | Leu | |
| 186 | | | | | 20 | | | 25 | | | | | | 30 | | | |
| 187 | Tyr | Met | Cys | Val | Cys | Glu | Gly | Leu | Ser | Cys | Gly | Asn | Glu | Asp | His | Cys | |
| 188 | | | | | 35 | | | 40 | | | | | | 45 | | | |
| 189 | Glu | Gly | Gln | Gln | Cys | Phe | Ser | Ser | Leu | Ser | Ile | Asn | Asp | Gly | Phe | His | |
| 190 | | | | | 50 | | | 55 | | | | | | 60 | | | |
| 191 | Val | Tyr | Gln | Lys | Gly | Cys | Phe | Gln | Val | Tyr | Glu | Gln | Gly | Lys | Met | Thr | |
| 192 | | | | | 65 | | | 70 | | | | | | 75 | | | 80 |
| 193 | Cys | Lys | Thr | Pro | Pro | Ser | Pro | Gly | Gln | Ala | Val | Glu | Cys | Cys | Gln | Gly | |
| 194 | | | | | | | | 85 | | | | | | 90 | | | 95 |

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 196 100 105 110
 197 Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
 198 115 120 125
 199 Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
 200 130 135 140
 201 Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
 202 145 150 155 160
 203 Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
 204 165 170 175
 205 Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
 206 180 185 190
 207 Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
 208 195 200 205
 209 Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
 210 210 215 220
 211 Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
 212 225 230 235 240
 213 Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
 214 245 250 255
 215 Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
 216 260 265 270
 217 Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
 218 275 280 285
 219 Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
 220 290 295 300
 221 Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
 222 305 310 315 320
 223 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
 224 325 330 335
 225 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
 226 340 345 350
 227 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
 228 355 360 365
 229 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
 230 370 375 380
 231 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
 232 385 390 395 400
 233 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
 234 405 410 415
 235 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
 236 420 425 430
 237 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
 238 435 440 445
 239 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
 240 450 455 460
 241 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
 242 465 470 475 480
 243 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/267,963D

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Input Set : N:\Crf4\04072003\I267963B.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 20
Seq#:26; Xaa Pos. 2,4,5
Seq#:43; Xaa Pos. 2,3,4,5,6
Seq#:44; Xaa Pos. 1,3,4,6

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

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L:7 M:270 C: Current Application Number differs, Wrong Format
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:1591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:1617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0